SEQUENCE LISTING

<110> GLIMCHER, LAURIE H.
DOUHAN III, JOHN

<120> HUMAN C-MAF COMPOSITIONS AND METHODS OF USE THEREFOR

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<141> 2001-06-12

<150> 09/086,010
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aaa aag gaa ccg gtg gag acc gac cgc atc atc agc cag tgc ggc cgt   144
Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
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ctc atc gcc ggg ggc tcg ctg tcc tcc acc ccc atg agc acg ccc tgc   192
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cga ggc gaa cag aag gcg cac ctg gaa gac tac tac tgg atg acc ggc   288
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tac ccg cag cag ctg aac ccc gag gcg ctg ggc ttc agc ccc gag gac   336
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Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
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Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
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Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
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Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
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Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
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Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
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aaa aag gaa ccg gtg gag acc gac cgc atc atc agc cag tgc ggc cgt  144
Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
         35                  40                  45

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ggc agc gaa cag aag gcg cac ctg gaa gac tac tac tgg atg acc ggc  288
Gly Ser Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
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gcg gtc gag gcg ctc atc agc aac agc cac cag ctc cag ggt ggc ttc  384
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gcc gcc gtg gtg tcc gcc gtg atc gcc gcg gcc gcc gcg cag agc ggc  528
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His His Pro Thr Ala Gly Ala Pro Gly Thr Ala Gly Gly Ala Ser Ser
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Ser Ser Asn Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Asn Thr
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225                 230                 235                 240
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ggc gcc ctt cac ccg cac cat tcc gcg ggc ggc ctg cac ttc gac gac   768
Gly Ala Leu His Pro His His Ser Ala Gly Gly Leu His Phe Asp Asp
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cgc ttc tcg gac gag cag ttg gtg acc atg tcg gtg cgc gaa ctg aac   816
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cgg cag ctg cgc ggg gtc agc aag gag gag gtg atc cga ctg aag cag   864
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aag agg cgg acc ctg aaa aac cgc ggc tat gcc cag tcc tgc cgc ttc   912
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aag agg gtg cag cag aga cac gtc ctg gag tcg gag aag aac cag ctg   960
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ctg cag cag gta gac cac ctc aag cag gag atc tcc agg ctg gtg cgc   1008
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Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
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Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
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Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
 65                  70                  75                  80
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Gly Ser Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
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Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
             100                 105                 110

Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Gln Gly Gly Phe
         115                 120                 125

Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
     130                 135                 140

Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
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Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly
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His His Pro Thr Ala Gly Ala Pro Gly Thr Ala Gly Gly Ala Ser Ser
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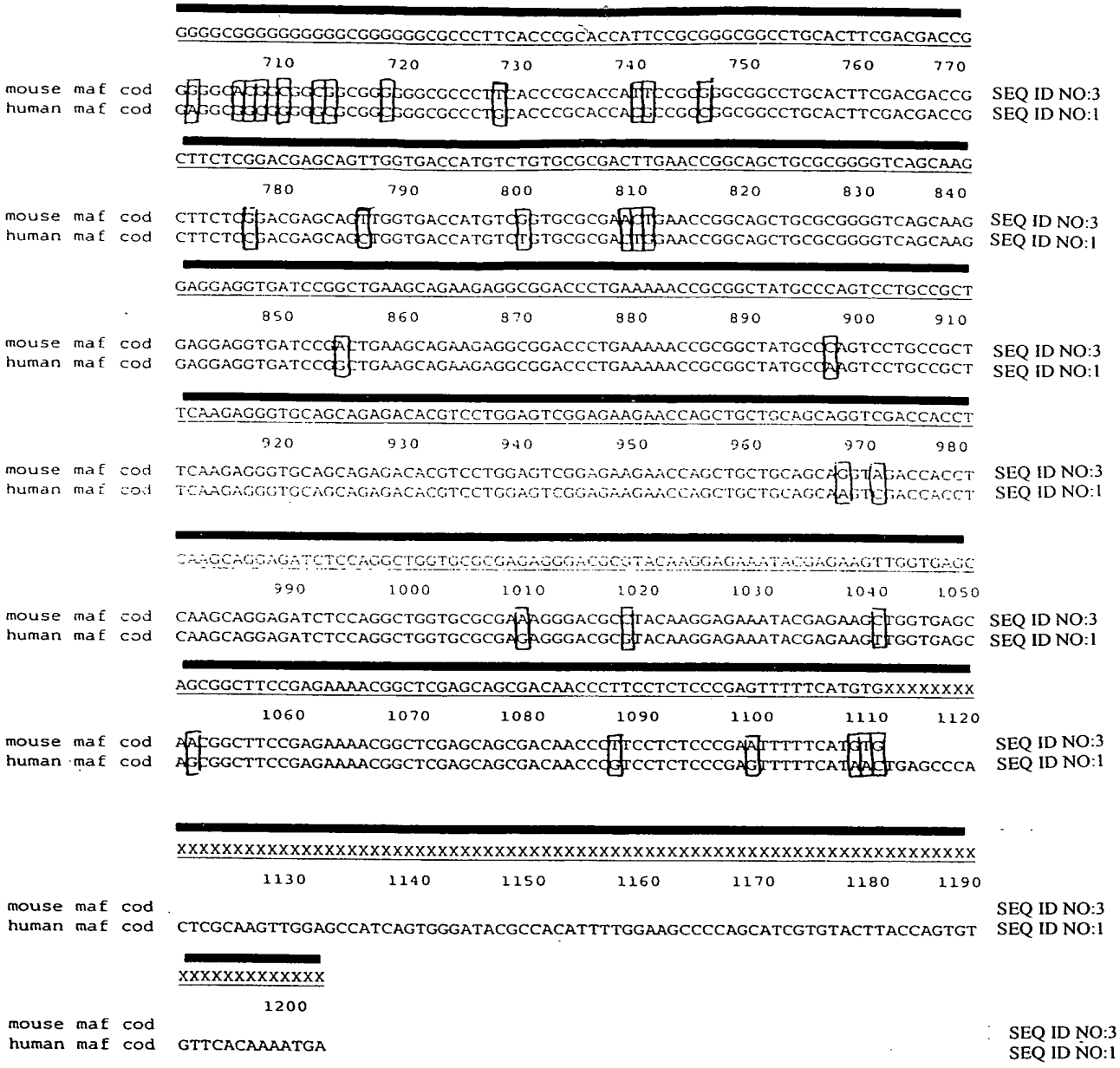
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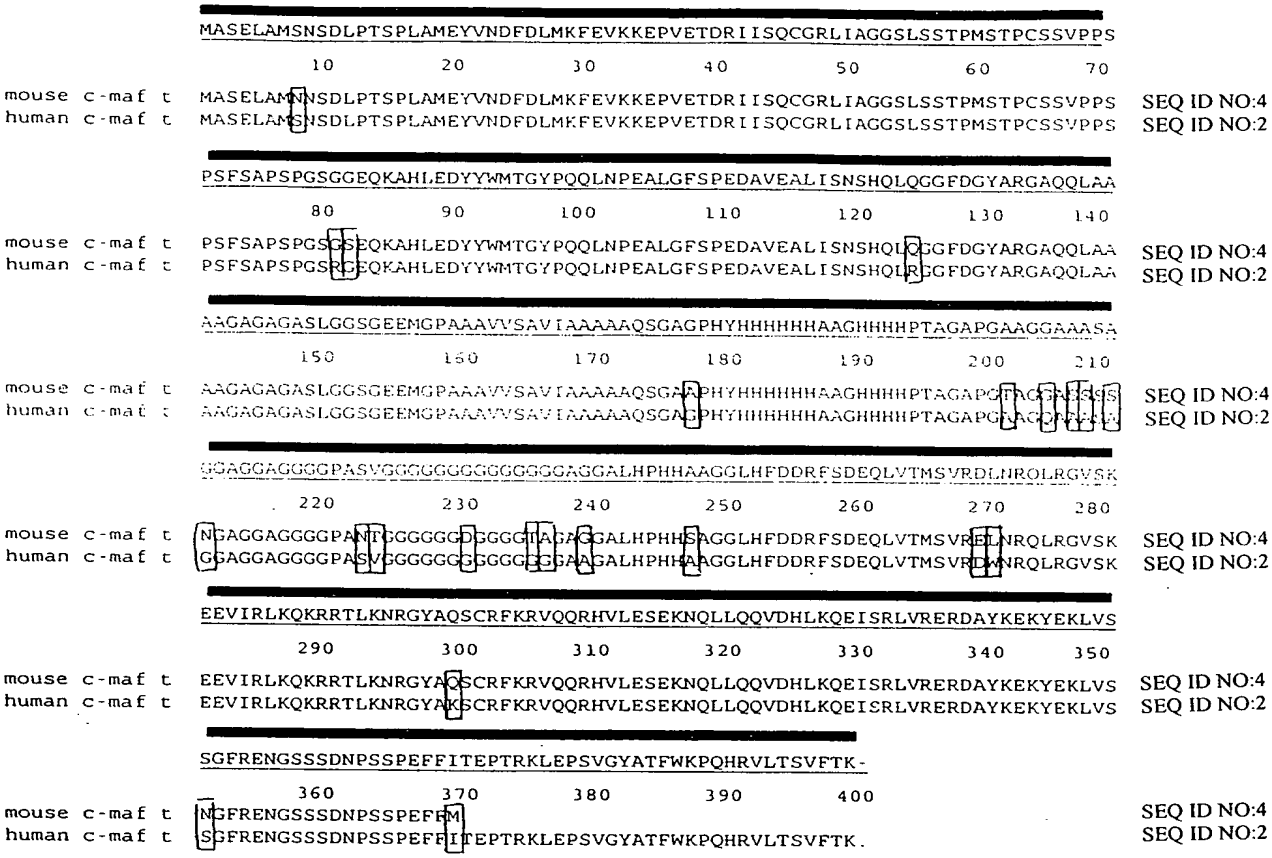
FIGURE 1B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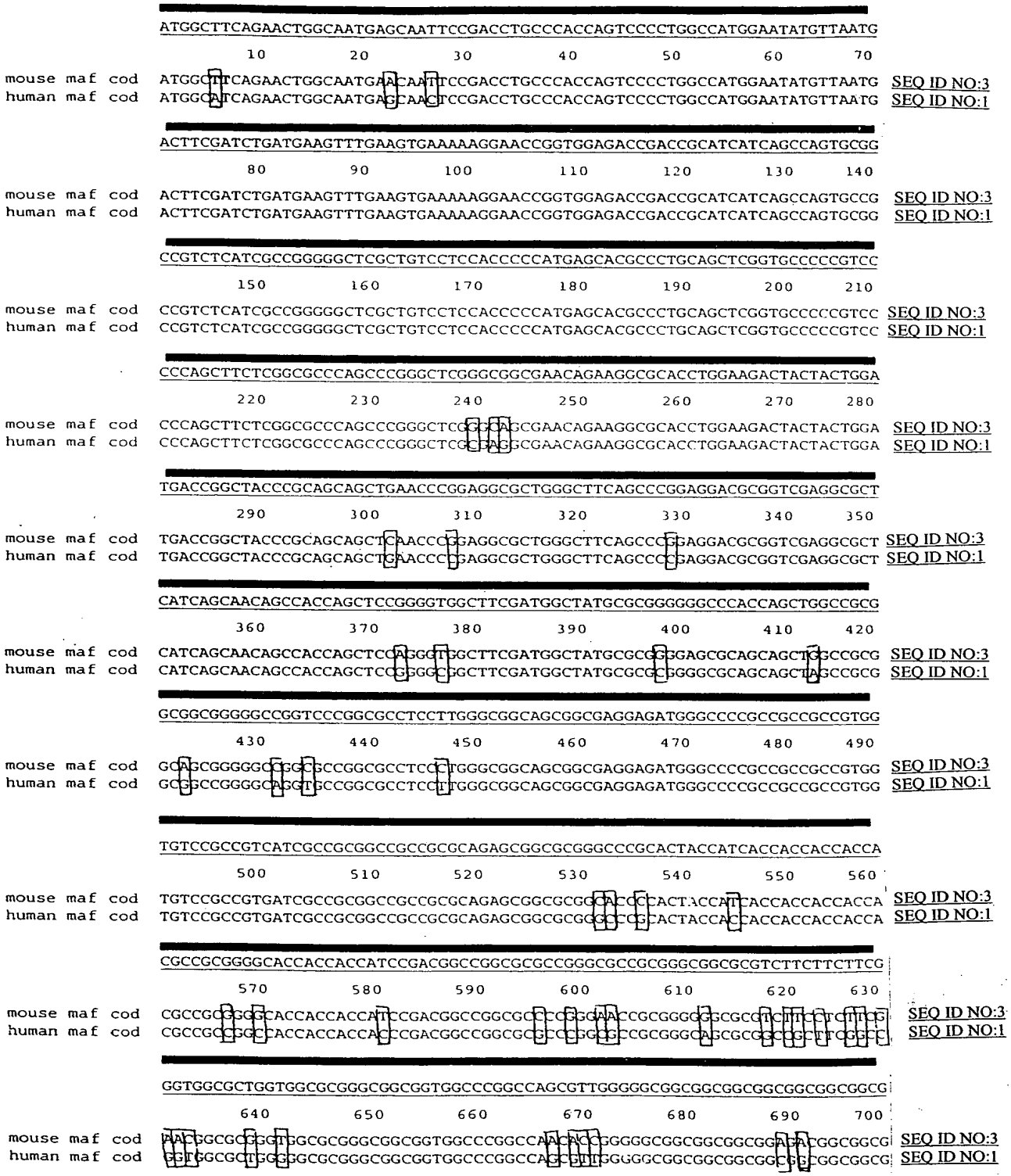
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80 90 100 110 120 130 140
mouse maf cod ACTTCGATCTGATGAAGTTTGAAGTGAAAAAGGAACCGGTGGAGACCGACCGCATCATCAGCCAGTGCCG SEQ ID NO:3
human maf cod ACTTCGATCTGATGAAGTTTGAAGTGAAAAAGGAACCGGTGGAGACCGACCGCATCATCAGCCAGTGCGG SEQ ID NO:1
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150 160 170 180 190 200 210
mouse maf cod CCGTCTCATCGCCGGGGGCTCGCTGTCCTCCACCCCCATGAGCACGCCCTGCAGCTCGGTGCCCCCGTCC SEQ ID NO:3
human maf cod CCGTCTCATCGCCGGGGGCTCGCTGTCCTCCACCCCCATGAGCACGCCCTGCAGCTCGGTGCCCCCGTCC SEQ ID NO:1
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220 230 240 250 260 270 280
mouse maf cod CCCAGCTTCTCGGCGCCCAGCCCGGGCTCGGGCGGCGAACAGAAGGCGCACCTGGAAGACTACTACTGGA SEQ ID NO:3
human maf cod CCCAGCTTCTCGGCGCCCAGCCCGGGCTCGGGCGGCGAACAGAAGGCGCACCTGGAAGACTACTACTGGA SEQ ID NO:1
TGACCGGCTACCCGCAGCAGCTGAACCCGGAGGCGCTGGGCTTCAGCCCGGAGGACGCGGTCGAGGCGCT
290 300 310 320 330 340 350
mouse maf cod TGACCGGCTACCCGCAGCAGCTCAACCCGGAGGCGCTGGGCTTCAGCCCGGAGGACGCGGTCGAGGCGCT SEQ ID NO:3
human maf cod TGACCGGCTACCCGCAGCAGCTGAACCCGGAGGCGCTGGGCTTCAGCCCGGAGGACGCGGTCGAGGCGCT SEQ ID NO:1
CATCAGCAACAGCCACCAGCTCCGGGGTGGCTTCGATGGCTATGCGCGGGGGGCCCACCAGCTGGCCGCG
360 370 380 390 400 410 420
mouse maf cod CATCAGCAACAGCCACCAGCTCCAGGGTGGCTTCGATGGCTATGCGCGGGGAGCGCAGCAGCTGGCCGCG SEQ ID NO:3
human maf cod CATCAGCAACAGCCACCAGCTCCGGGGCGGCTTCGATGGCTATGCGCGCGGGGCGCAGCAGCTAGCCGCG SEQ ID NO:1
GCGGCGGGGGCCGGTCCCGGCGCCTCCTTGGGCGGCAGCGGCGAGGAGATGGGCCCCGCCGCCGCCGTGG
430 440 450 460 470 480 490
mouse maf cod GCAGCGGGGGCCGGCGCCGGCGCCTCCTTGGGCGGCAGCGGCGAGGAGATGGGCCCCGCCGCCGCCGTGG SEQ ID NO:3
human maf cod GCGGCCGGGGCAGGTGCCGGCGCCTCCTTGGGCGGCAGCGGCGAGGAGATGGGCCCCGCCGCCGCCGTGG SEQ ID NO:1
TGTCCGCCGTCATCGCCGCGGCCGCCGCGCAGAGCGGCGCGGGCCCGCACTACCATCACCACCACCACCA
500 510 520 530 540 550 560
mouse maf cod TGTCCGCCGTGATCGCCGCGGCCGCCGCGCAGAGCGGCGCGGCACCCCACTACCATCACCACCACCACCA SEQ ID NO:3
human maf cod TGTCCGCCGTGATCGCCGCGGCCGCCGCGCAGAGCGGCGCGGGCCCGCACTACCACCACCACCACCA SEQ ID NO:1
CGCCGCGGGGCACCACCACCATCCGACGGCCGGCGCGCCGGGCGCCGCGGGCGGCGCGTCTTCTTCTTCG
570 580 590 600 610 620 630
mouse maf cod CGCCGCGGGGCACCACCACCATCCGACGGCCGGCGCCCCGGGAACCGCGGGGGGCGCGTCTTCTTCTTCG SEQ ID NO:3
human maf cod CGCCGCGGGCCACCACCACCACCCGACGGCCGGCGCGCCGGGGCCGCGGGCAGCGCGGCGCTTCGGCTC SEQ ID NO:1
GGTGGCGCTGGTGGCGCGGGCGGCGGTGGCCCGGCCAGCGTTGGGGGCGGCGGCGGCGGCGGCGGCG
640 650 660 670 680 690 700
mouse maf cod AACGGCGCGGGTGGCGCGGGCGGCGGTGGCCCGGCCAACACCGGGGGCGGCGGCGGCGGCGGCGGCG SEQ ID NO:3
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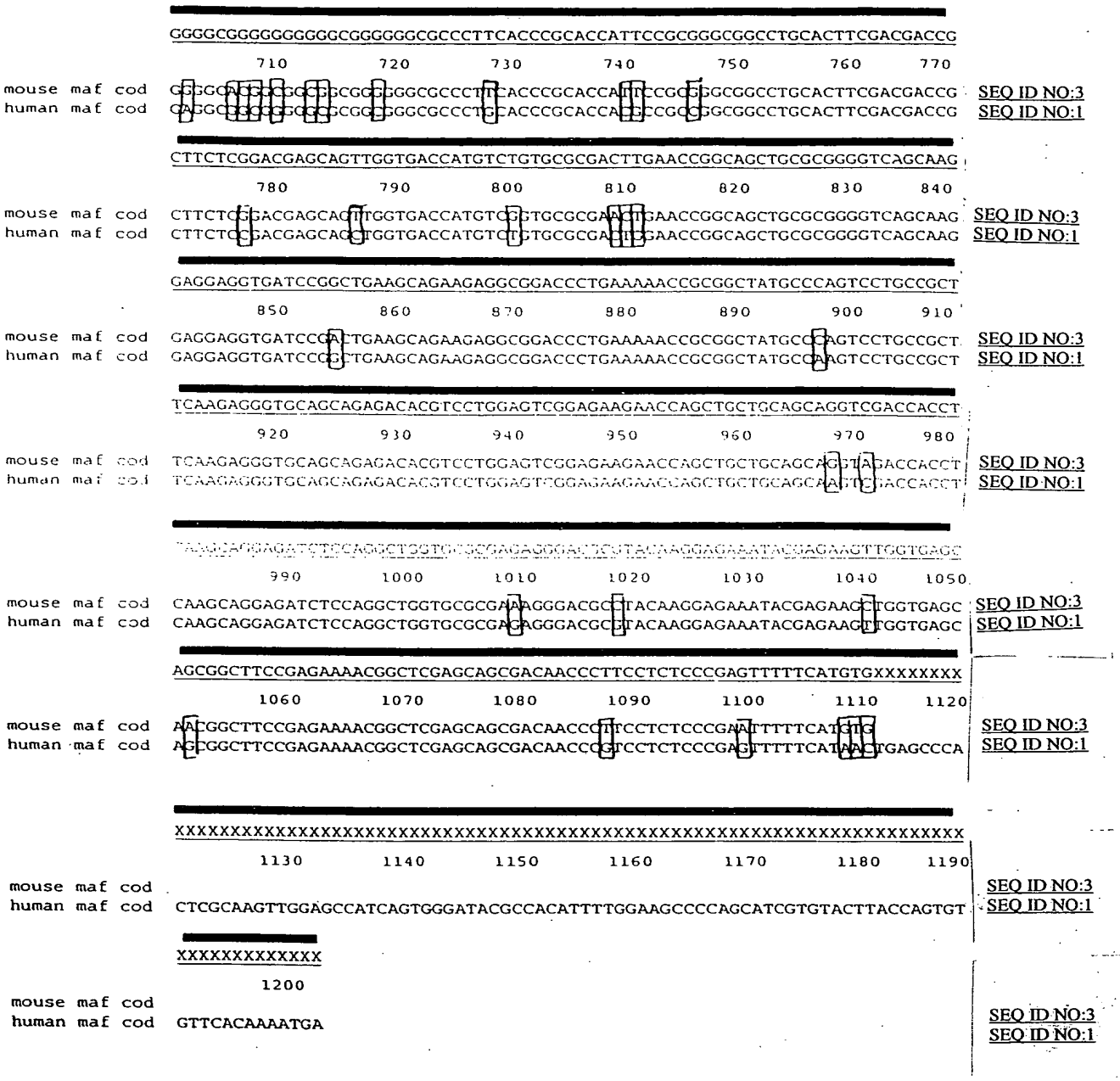
FIGURE 1A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mouse maf cod
human maf cod
SEQ ID NO:3
SEQ ID NO:1
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780 790 800 810 820 830 840
mouse maf cod
human maf cod
SEQ ID NO:3
SEQ ID NO:1
GAGGAGGTGATCCGGCTGAAGCAGAAGAGGCGGACCCTGAAAAACCGCGGCTATGCCCAGTCCTGCCGCT
850 860 870 880 890 900 910
mouse maf cod
human maf cod
SEQ ID NO:3
SEQ ID NO:1
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920 930 940 950 960 970 980
mouse maf cod
human maf cod
SEQ ID NO:3
SEQ ID NO:1
990 1000 1010 1020 1030 1040 1050
mouse maf cod
human maf cod
SEQ ID NO:3
SEQ ID NO:1
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1060 1070 1080 1090 1100 1110 1120
mouse maf cod
human maf cod
SEQ ID NO:3
SEQ ID NO:1
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
1130 1140 1150 1160 1170 1180 1190
mouse maf cod
human maf cod
CTCGCAAGTTGGAGCCATCAGTGGGATACGCCACATTTTGGAAGCCCCAGCATCGTGTACTTACCAGTGT
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SEQ ID NO:1
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mouse maf cod
human maf cod
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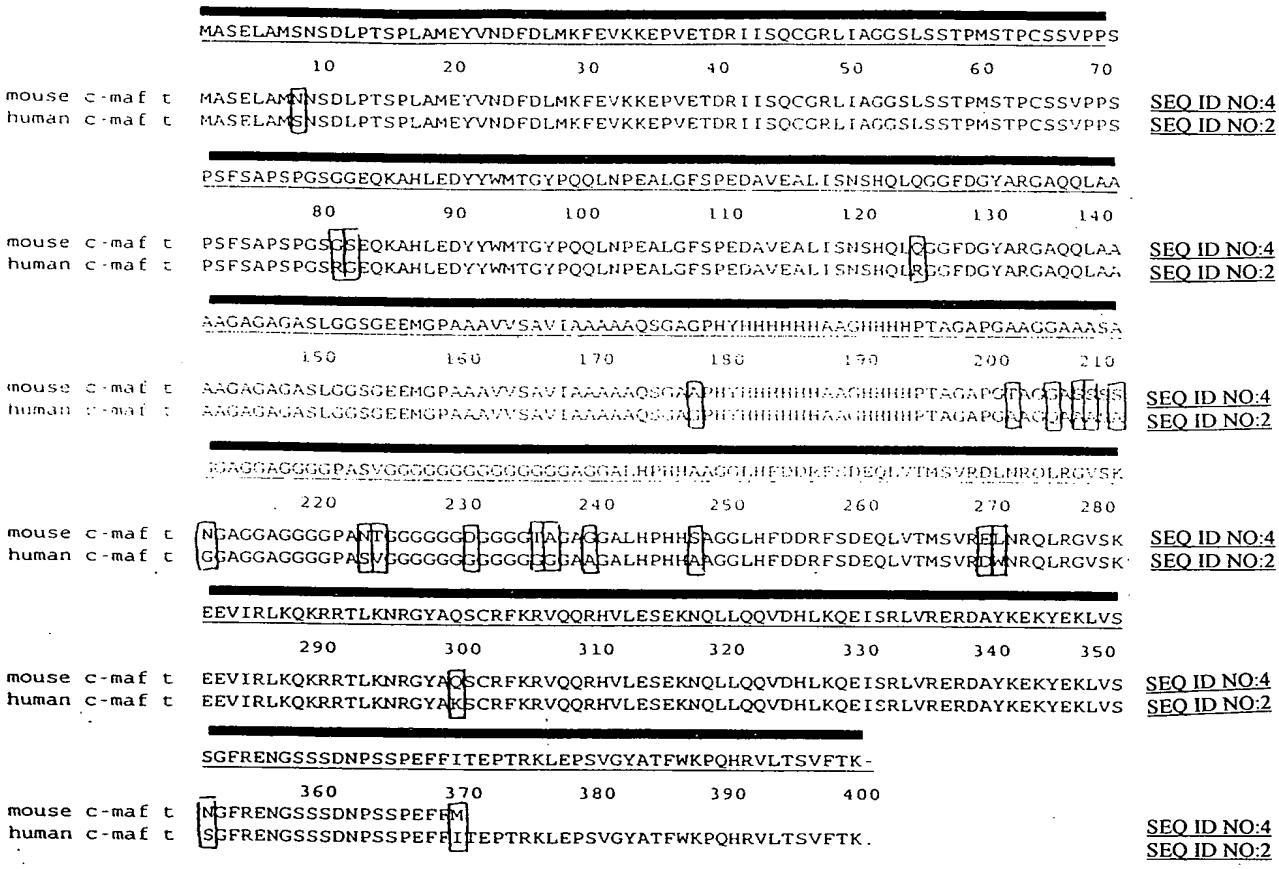
SEQ ID NO:3
SEQ ID NO:1

FIGURE 1B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human c-maf t MASELAMSNSDLPTSPLAMEYVNDFDLMKFEVKKEPVETDRIISQCGRLIAGGSLSSTPMSTPCSSVPPS SEQ ID NO:2
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80 90 100 110 120 130 140
mouse c-maf t PSFSAPSPGSGSEQKAHLEDYYWMTGYPQQLNPEALGFSPEDAVEALISNSHQLQGGFDGYARGAQQLAA SEQ ID NO:4
human c-maf t PSFSAPSPGSRSEQKAHLEDYYWMTGYPQQLNPEALGFSPEDAVEALISNSHQLRGGFDGYARGAQQLAA SEQ ID NO:2
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150 160 170 180 190 200 210
mouse c-maf t AAGAGAGASLGGSGEEMGPAAAVVSAVIAAAAAQSGAGPHYHHHHHHAAGHHHHPTAGAPGAAGGAAASA SEQ ID NO:4
human c-maf t AAGAGAGASLGGSGEEMGPAAAVVSAVIAAAAAQSGAGPHYHHHHHHAAGHHHHPTAGAPGAAGGAAASA SEQ ID NO:2
NGAGGAGGGGPASVGGGGGGGGGGGGGGAGGALHPHHAAGGLHFDDRFSDEQLVTMSVRELNRQLRGVSK
220 230 240 250 260 270 280
mouse c-maf t NGAGGAGGGGPANTGGGGGGDGGGGHAGAGGALHPHHSAGGLHFDDRFSDEQLVTMSVRELNRQLRGVSK SEQ ID NO:4
human c-maf t GGAGGAGGGGPASVGGGGGGGGGGGGGGAGGALHPHHAAGGLHFDDRFSDEQLVTMSVRDLNRQLRGVSK SEQ ID NO:2
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290 300 310 320 330 340 350
mouse c-maf t EEVIRLKQKRRTLKNRGYAQSCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKEKYEKLVS SEQ ID NO:4
human c-maf t EEVIRLKQKRRTLKNRGYAKSCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKEKYEKLVS SEQ ID NO:2
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360 370 380 390 400
mouse c-maf t NGFRENGSSSDNPSSPEFFM
human c-maf t SGFRENGSSSDNPSSPEFFITEPTRKLEPSVGYATFWKPQHRVLTSVFTK. SEQ ID NO:4 SEQ ID NO:2

FIGURE 2